

9/937076

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:47:04 ; Search time 16 Seconds
(without alignments)
48.096 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 19 | 44.2 | 7 | S71299 | ICL2 protein - Par |
| 2 | 19 | 44.2 | 7 | PT0283 | Ig heavy chain CRD |
| 3 | 16 | 37.2 | 5 | B37988 | acid proteinase li |
| 4 | 16 | 37.2 | 8 | B24749 | neuropeptide B - b |
| 5 | 16 | 37.2 | 8 | B39745 | endoglycosylcerami |
| 6 | 15 | 34.9 | 7 | A61081 | tryptophyllin, bas |
| 7 | 15 | 34.9 | 7 | A39690 | neural cell adhesi |
| 8 | 15 | 34.9 | 7 | S15597 | orf 4 rara 5'-regi |
| 9 | 14 | 32.6 | 8 | S16324 | hypothetical prote |
| 10 | 14 | 32.6 | 8 | S21288 | lectin - potato (f |
| 11 | 14 | 32.6 | 8 | PT0030 | inulinase (EC 3.2. |
| 12 | 14 | 32.6 | 8 | E47393 | neuropeptide calla |
| 13 | 14 | 32.6 | 8 | S10783 | enamelin f - bovin |
| 14 | 14 | 32.6 | 8 | PT0559 | T-cell receptor be |
| 15 | 13 | 30.2 | 8 | S22428 | chitin-binding pro |
| 16 | 13 | 30.2 | 8 | S14895 | apolipoprotein A-I |
| 17 | 12 | 27.9 | 4 | A02147 | phagocytosis-stimu |
| 18 | 12 | 27.9 | 5 | B22565 | R-phycoerythrin al |
| 19 | 12 | 27.9 | 6 | B60110 | repetitive protein |
| 20 | 12 | 27.9 | 6 | A11490 | pyruvate kinase (E |
| 21 | 12 | 27.9 | 6 | PT0618 | T-cell receptor be |
| 22 | 12 | 27.9 | 7 | A44428 | platelet aggregati |
| 23 | 12 | 27.9 | 7 | PC1316 | large granule L3 c |
| 24 | 12 | 27.9 | 7 | S42620 | aggrecan - bovine |
| 25 | 12 | 27.9 | 7 | A58718 | carnocin UR49 - Ca |
| 26 | 12 | 27.9 | 8 | S43971 | tumor-associated a |
| 27 | 12 | 27.9 | 8 | A23967 | leucopyrokinin - M |
| 28 | 12 | 27.9 | 8 | S66646 | cardioacceleratory |
| 29 | 12 | 27.9 | 8 | A14683 | aspartate transami |

| | | | | | | |
|----|----|------|---|---|--------|--------------------|
| 30 | 12 | 27.9 | 8 | 2 | A61457 | penalbumin - Adeli |
| 31 | 12 | 27.9 | 8 | 2 | PT0691 | T-cell receptor be |
| 32 | 12 | 27.9 | 8 | 2 | A39690 | neural cell adhesi |
| 33 | 11 | 25.6 | 3 | 3 | A33802 | thyrotropin-releas |
| 34 | 11 | 25.6 | 3 | 3 | S68328 | blood cell protein |
| 35 | 11 | 25.6 | 5 | 2 | JN0860 | peptidyl-dipeptida |
| 36 | 11 | 25.6 | 5 | 2 | PS0324 | ribulose-bisphosph |
| 37 | 11 | 25.6 | 5 | 2 | S55237 | zinc-binding prote |
| 38 | 11 | 25.6 | 5 | 3 | UT0870 | phytoaulfokine alp |
| 39 | 11 | 25.6 | 6 | 2 | S66195 | alcohol dehydrogen |
| 40 | 11 | 25.6 | 6 | 2 | A37765 | hypothetical prote |
| 41 | 11 | 25.6 | 6 | 2 | PC4127 | hypothetical 6 pro |
| 42 | 11 | 25.6 | 6 | 2 | A19780 | transferrin - bovi |
| 43 | 11 | 25.6 | 7 | 1 | NYPG7 | hypothalamic hepta |
| 44 | 11 | 25.6 | 7 | 2 | A25269 | sex pheromone cAm3 |
| 45 | 11 | 25.6 | 7 | 2 | PH0932 | T-cell receptor be |

ALIGNMENTS

RESULT 1

S71299 ICL2 protein - Paramedium tetraurelia (fragment)
C:Species: Paramedium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R.Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramedium.
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match 44.2%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
DB 2 QPP 4

RESULT 2

PT0283 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0282; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 44.2%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
DB 5 QPP 7

RESULT 3

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C>Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og
J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase from
A:Reference number: A37988; MUID:91060608; PMID:2246266
A:Accession: B37988
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MOR>

Query Match 37.2%; Score 16; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
:||
DB 2 EPP 4

RESULT 4
B24749
neuropeptide B - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C:Accession: B24749
R:Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
A:Reference number: A94074; MUID:86067985; PMID:3865193
A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <YAN>
A:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match 37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
:||
DB 4 QPQR 7

RESULT 5
B39745
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)
C:Species: Rhodococcus sp.
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-1993
C:Accession: B39745
R:Itto, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. E
ble using these activator proteins.

A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: B39745
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <ITO>
C:Keywords: glycosidase; hydrolase

Query Match 37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PRA 5
:||
DB 6 PRA 8

RESULT 6

A61081
tryptophyllin, basic - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:Accession: A61081
R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
Int. J. Pept. Protein Res. 33, 391-395, 1989
A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containi
A:Reference number: A61081
A:Accession: A61081
A:Molecule type: protein
A:Residues: 1-7 <MON>

A:Comment: The biological activity of this peptide was not determined.
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; hydroxyproline; skin
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 34.9%; Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
:||
DB 1 KPP 3

RESULT 7

A39690
neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: A39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule nR
A:Reference number: A39690; MUID:91141516; PMID:11961115
A:Accession: A39690
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-7 <REY>
A:Cross-references: GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 34.9%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
:||
DB 1 QPVR 4

RESULT 8

S15597
orf 4 para 5'-region - human
C:Species: Homo sapiens (man)
C>Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15597
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15597
A:Molecule type: DNA
A:Residues: 1-7 <BRA>

A:Cross-references: EMBL:X56058; NID:g35876
A>Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240
A;Map position: 17q12-17q12

Query Match 34.9%; Score 15; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PRAAI 7
|||
Db 2 PRGV 6

RESULT 9

S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <NRUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 7 PP 8

RESULT 10

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C;Accession: S21288
R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Siabias, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A;Reference number: S21288; MUID:92272683; PMID:1590771
A;Accession: S21288
A;Molecule type: protein
A;Residues: 1-8 <ML>
A;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 7 PP 8

RESULT 11

PT0030
inulinase (EC 3.2.1.7) - Aspergillus ficum (fragment)
N;Alternate names: inulase
C;Species: Aspergillus ficum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
C;Accession: PT0030
R;Etcalibi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990

A;Title: Molecular and kinetic properties of Aspergillus ficum inulinases.
A;Reference number: PT0030; MUID:90344234; PMID:1368526
A;Accession: PT0030
A;Molecule type: protein
A;Residues: 1-8 <FTT>
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
|||
Db 5 QPYR 8

RESULT 12

E47393
neuropeptide callatostatatin 5 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence
A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Experimental source: whole flies
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 2 PP 3

RESULT 13

S10783
enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albi
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 4 PP 5

RESULT 14

PT0559
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0559
R;Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: F10509; MUID:91277601; PMID:1711558
 A;Accession: F10559
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-8 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 pp 3
 ||
 Db 4 pp 5

RESULT 15
 S22428
 chitin-binding protein - potato (fragment)
 C;Species: Solanum tuberosum (potato)
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C;Accession: S22428
 R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
 A;Reference number: S21286; MUID:92272683; PMID:1590771
 A;Accession: S22428
 A;Molecule type: protein
 A;Residues: 1-8 <MIL>
 C;Function:
 A;Description: may be involved in plant defence
 C;Keywords: glycoprotein; hydroxyproline

Query Match 30.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. NO. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 PRAAY 8
 | : |
 Db 1 PXDMVY 6

Search completed: July 28, 2004, 07:55:22
 Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:17:39 ; Search time 13 Seconds
(without alignments)
32.043 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|---------------|---------------------|
| 1 | 16 | 37.2 | 8 | 1 NPMB_BOVIN | P15507 bos taurus |
| 2 | 15 | 34.9 | 7 | 1 TPFY_PACDA | P83455 pachymedusa |
| 3 | 15 | 34.9 | 7 | 1 UPO4_MOUSE | P38642 mus musculus |
| 4 | 15 | 34.9 | 8 | 1 PPK2_PERAM | P82692 periplaneta |
| 5 | 14 | 32.6 | 8 | 1 ALL5_CALVO | P41841 calliphora |
| 6 | 12 | 27.9 | 4 | 1 TUFT_HUMAN | P01858 homo sapien |
| 7 | 12 | 27.9 | 7 | 1 LANC_CARUI | P36960 carnobacter |
| 8 | 12 | 27.9 | 8 | 1 FAR7_ASCSU | P43171 ascaris suu |
| 9 | 12 | 27.9 | 8 | 1 LMT2_LOCOMI | P22396 locusta mig |
| 10 | 12 | 27.9 | 8 | 1 LPK_LEUMA | P13049 leucophaea |
| 11 | 12 | 27.9 | 8 | 1 PPK3_PERAM | P82618 periplaneta |
| 12 | 12 | 27.9 | 8 | 1 RS7_MYCIT | P33564 mycobacteri |
| 13 | 12 | 27.9 | 8 | 1 UC25_MAIZE | P80632 zea mays (m |
| 14 | 12 | 27.9 | 8 | 1 UPAT_HUMAN | P30087 homo sapien |
| 15 | 11 | 25.6 | 5 | 1 PSK_DAUCA | P58261 daucus caro |
| 16 | 11 | 25.6 | 7 | 1 CIA_ENTFA | P11932 enterococcu |
| 17 | 11 | 25.6 | 7 | 1 BI05_LITRU | P82101 litoria rub |
| 18 | 11 | 25.6 | 7 | 1 HV7_PIG | P01153 sus scrofa |
| 19 | 11 | 25.6 | 8 | 1 UH05_RAT | P56575 rattus norv |
| 20 | 10 | 23.3 | 3 | 1 THYL_PIG | P01151 sus scrofa |
| 21 | 10 | 23.3 | 8 | 1 ANG2_BORJA | Q10582 bothrops ja |
| 22 | 9 | 20.9 | 7 | 1 ALL3_CARMA | P81806 carcinus ma |
| 23 | 9 | 20.9 | 7 | 1 ALL4_CARMA | P81807 carcinus ma |
| 24 | 9 | 20.9 | 7 | 1 ALL5_CARMA | P81808 carcinus ma |
| 25 | 9 | 20.9 | 7 | 1 MNP1_LEPDE | P42984 leptinotars |
| 26 | 9 | 20.9 | 7 | 1 TV51_LITRU | P82055 litoria rub |
| 27 | 9 | 20.9 | 7 | 1 UN06_PINPS | P81675 pinus pinas |
| 28 | 9 | 20.9 | 8 | 1 ALL6_CYPDO | P82157 cydia pomon |
| 29 | 9 | 20.9 | 8 | 1 ALL7_CARMA | P81809 carcinus ma |
| 30 | 9 | 20.9 | 8 | 1 ALL8_CARMA | P81811 carcinus ma |
| 31 | 9 | 20.9 | 8 | 1 ALL9_CARMA | P81812 carcinus ma |
| 32 | 9 | 20.9 | 8 | 1 LCK8_LEUMA | P19990 leucophaea |
| 33 | 9 | 20.9 | 8 | 1 NS3_MYCTU | P81152 mycobacteri |

ALIGNMENTS

RESULT 1

NPMB_BOVIN
ID NPMB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Morphine modulating neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: Modulates the action of morphine.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
Query Match 37.2%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4

Db 4 QPQR 7

RESULT 2

TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (pdt-1).
OS Pachymedusa dactylos (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE-Skin secretion;
RC Chen T.B., Orr D.F., Shaw C.;

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RT "Pachymedusa daemnicolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
Db :||
1 KPP 3

RESULT 3
UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Sellkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 46 kDa.
FT NON_TER 7
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
Db :||
2 KPP 4

RESULT 4
PPK2_PERAM STANDARD; PRT; 8 AA.
AC P22692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (pea-pk-2) (FXPR1-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR Neuropeptide; Amidation; Hydroxylation.
KW NCBI_TaxID=6978;
FT MOD_RES 3 3 HYDROXYLATION (20%).

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RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FxPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPRA 5
Db :||
2 PPFA 5

RESULT 5
ALLS_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatin.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR Neuropeptide; Amidation; Hydroxylation.
KW NCBI_TaxID=27454;
FT MOD_RES 3 3 HYDROXYLATION (20%).

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FT  MOD RES      8      8      AMIDATION
SQ  SEQUENCE  8 AA,  883 MW,  7D9879CABB477768 CRC64;

Query Match      32.6%; Score 14; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 PP 3
Db  2 PP 3

RESULT 6
TUFT HUMAN
ID  _TUFT_HUMAN  STANDARD; PRT; 4 AA.
AC  P01858;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Phagocytosis-stimulating peptide (Tuftsin).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=72187087; PubMed=4112769;
RA  Nishioka K., Constantopoulos A., Satch P.S., Najjar V.A.;
RT  "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL  Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN  [2]
RP  IMMUNOGLOBULIN CLASS.
RX  MEDLINE=68091045; PubMed=4169272;
RA  Fidalco B.V., Najjar V.A.;
RT  "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL  Biochemistry 6:3386-3392(1967).
CC  -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
cell membrane of neutrophils in the blood. Leucokininase on the
membrane releases the active peptide tuftsin from the gamma chain.
CC  Tuftsin is essential for maximum stimulation of the phagocytic
activity of neutrophils.
DR  PIR; A02147; A02147.
DR  MIN; 191150; -.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006909; P:phagocytosis; NAS.
SQ  SEQUENCE 4 AA, 501 MW, 74176321C0000000 CRC64;

Query Match      27.9%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PR 4
Db  3 PR 4

RESULT 7
LANC CARUI
ID  _LANC_CARUI  STANDARD; PRT; 7 AA.
AC  P36960;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Lantibiotic carnocin U149 (Fragment).
OS  Carnobacterium sp. (strain U149).
OC  Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC  Carnobacterium.
OX  NCBI_TaxID=35782;
RN  [1]
RP  SEQUENCE.

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RX  MEDLINE=92321768; PubMed=1622206;
RA  Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA  Nes I.F.;
RT  "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
RL  Appl. Environ. Microbiol. 58:1417-1422(1992).
-!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC  Active on Gram-positive bacteria.
KW  Antibiotic; Bacteriocin; Lantibiotic.
FT  NON_TER 7
SQ  SEQUENCE 7 AA, 786 MW, 741776D05B05B810 CRC64;

Query Match      27.9%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QP 2
Db  5 QP 6

RESULT 8
FAR7 ASCSU
ID  _FAR7_ASCSU  STANDARD; PRT; 8 AA.
AC  F43171;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  FMRamide-like neuropeptide AF7.
OS  Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC  Ascarididae; Ascaris.
OX  NCBI_TaxID=6253;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=95380362; PubMed=7651904;
RA  Cowden C., Stretton A.O.W.;
RT  "Eight novel FMRamide-like neuropeptides isolated from the nematode
Ascaris suum.";
RL  Peptides 16:491-500(1995).
CC  -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW  Neuropeptide; Amidation.
FT  MOD_RES 8
SQ  SEQUENCE 8 AA, 963 MW, 9CD40059D417687D CRC64;

Query Match      27.9%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PR 4
Db  3 PR 4

RESULT 9
LMT2 LOCM1
ID  _LMT2_LOCM1  STANDARD; PRT; 8 AA.
AC  P22396;
DT  01-AUG-1991 (Rel. 19, Created)
DT  01-AUG-1991 (Rel. 19, Last sequence update)
DT  01-AUG-1991 (Rel. 19, Last annotation update)
DE  Locustamyotropin 2 (LOM-MT-2).
OS  Locusta migratoria (Migratory locust).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC  Acridoidea; Acrididae; Oedipodinae; Locusta.
OX  NCBI_TaxID=7004;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Corpora cardiaca;
RA  Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT  "Isolation, identification and synthesis of locustamyotropin II, an

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RT additional neuropeptide of Locusta migratoria. Member of the
 RL cephalomyotropic peptide family.";
 CC Insect Biochem. 20:479-484(1990).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
 Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PR 4
 DB 6 PR 7

RESULT 10
 LPK_LEUMA
 ID LPK_LEUMA STANDARD; PRT; 8 AA.
 AC P13049;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leukopyrokinin (LPK) (LEM-PK).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 CC Blaberidae; Leucophaea.
 CC NCBI_TaxID=62988;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=86269041; PubMed=3015140;
 RA Nachman R.J., Holman G.M., Cook B.J.,
 RT "Active fragments and analogs of the insect neuropeptide
 RT leucopyrokinin: structure-function studies."
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
 RN [2]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA MEDLINE=87052651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of a blocked myotropic
 RT neuropeptide isolated from the cockroach, Leucophaea maderae."
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- MISCELLANEOUS: An analog without the N-terminal PCA residue was
 CC synthesized and found to exhibit greater activity (144%) than the
 CC parent neuropeptide. The portion of the sequence of LPK most
 CC critical for the myotropic properties is limited to the
 CC pentapeptide fragment FTPEPL.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR PIR; A23967; A23967.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1
 FT MOD_RES 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;
 Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PR 4
 DB 6 PR 7

RESULT 11
 PPK3_PERAM
 ID PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 CC Blattidae; Periplaneta.
 CC NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the Pyrokinin family.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;
 Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PR 4
 DB 6 PR 7

RESULT 12
 RST_MYCIT
 ID RST_MYCIT STANDARD; PRT; 8 AA.
 AC P33564;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7 (Fragment).
 GN RPSG.
 OS Mycobacterium intracellulare.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 CC NCBI_TaxID=1767;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93197130; PubMed=9451173;
 RA Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of
 RT Mycobacterium intracellulare."
 RL Nucleic Acids Res. 21:1039-1039(1993).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (by similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9


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CC and S11 (By similarity).
CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EVBL; L08171; AAA25376.1; -.
DR PIR; S35538; S35538.
DR HAVAP; MF 00480; -.
DR InterPro; IPR000235; Ribosomal S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
FT SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;
SQ
Query Match 27.9%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PR 4
DB 1 PR 2
RESULT 13
UC26_MAIZE
ID UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 7.0, its MW is: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
FT SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
SQ
Query Match 27.9%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PR 4
DB 3 PR 4
RESULT 14
UPA1_HUMAN
ID UPA1_HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)

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DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=9309937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RA "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.9, its MW is: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1 1
FT NON_TER 8 8
FT SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
SQ
Query Match 27.9%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PR 4
DB 7 PR 8
RESULT 15
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) (Contains: Phytosulfokine-beta (PSK-
DE beta)).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Apiales; Apiaceae; Scandiceae; Daucinae;
OC Daucus.
OC NCBI_TaxID=4039;
RN [1]
RP SEQUENCES, AND IDENTIFICATION BY MASS SPECTROMETRY.
RX STRAIN=cv. US-Harumakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kamada H., Sakagami Y.;
RA "A secreted peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -!- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
CC cells, but does not stimulate differentiation into the somatic
CC embryos.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Sulfation is important for activity and for the binding to a
CC putative membrane receptor (By similarity).
CC -!- SIMILARITY: Belongs to the phytosulfokine family.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
FT SEQUENCE 5 AA; 687 MW; 76C1BB504B3C0000 CRC64;
SQ
Query Match 25.6%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 7 IV 8
||
Db 2 IV 3

Search completed: July 28, 2004, 07:54:11
Job time : 14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2004, 07:43:54 ; Search time 34 Seconds
(without alignments)
74.240 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qprraaiy 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp Vertebrate:
- 14: sp Unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 16 | 37.2 | 7 | 8 P92214 | P92214 amblyopyrum |
| 2 | 16 | 37.2 | 7 | 8 P92393 | P92393 hordeum vul |
| 3 | 16 | 37.2 | 7 | 8 P92403 | P92403 lophopyrum |
| 4 | 16 | 37.2 | 7 | 8 P92427 | P92427 peridictyon |
| 5 | 16 | 37.2 | 7 | 8 P92430 | P92430 aegilops ta |
| 6 | 16 | 37.2 | 7 | 8 P92221 | P92221 bromus iner |
| 7 | 16 | 37.2 | 7 | 8 P92425 | P92425 pseudoroegn |
| 8 | 16 | 37.2 | 7 | 8 P92381 | P92381 hordeum bra |
| 9 | 16 | 37.2 | 7 | 8 P92387 | P92387 henrardia p |
| 10 | 16 | 37.2 | 7 | 8 P92210 | P92210 agropyron c |
| 11 | 16 | 37.2 | 7 | 8 P92440 | P92440 chinopyrum |
| 12 | 16 | 37.2 | 7 | 8 P92218 | P92218 australopyr |
| 13 | 16 | 37.2 | 7 | 8 P92390 | P92390 heteranthel |
| 14 | 16 | 37.2 | 7 | 8 P92372 | P92372 haynaldia v |
| 15 | 16 | 37.2 | 7 | 8 P92442 | P92442 taenitheru |
| 16 | 16 | 37.2 | 7 | 8 P92226 | P92226 crithopsis |

| | | | | | |
|----|----|------|---|-----------|--------------------|
| 17 | 16 | 37.2 | 7 | 8 P92385 | P92385 hordeum mar |
| 18 | 16 | 37.2 | 7 | 8 P92421 | P92421 psathyrosta |
| 19 | 16 | 37.2 | 8 | 11 Q9JLD7 | Q9JLD7 mesocricetu |
| 20 | 15 | 34.9 | 8 | 8 Q9GCZ4 | Q9GCZ4 nenga pumil |
| 21 | 15 | 34.9 | 8 | 8 Q9GD00 | Q9GD00 masoala mad |
| 22 | 15 | 34.9 | 8 | 8 Q9GD47 | Q9GD47 hydriastele |
| 23 | 14 | 32.6 | 8 | 12 Q9J205 | Q9J205 hepatitis c |
| 24 | 13 | 30.2 | 7 | 2 Q50556 | Q50556 actinobacil |
| 25 | 13 | 30.2 | 8 | 4 Q15900 | Q15900 homo sapien |
| 26 | 13 | 30.2 | 8 | 5 Q94623 | Q94623 manduca sex |
| 27 | 13 | 30.2 | 8 | 11 Q62528 | Q62528 mus spratus |
| 28 | 12 | 27.9 | 7 | 12 Q66113 | Q66113 cherry leaf |
| 29 | 12 | 27.9 | 8 | 2 Q56759 | Q56759 xanthobacte |
| 30 | 12 | 27.9 | 8 | 2 Q9RQ57 | Q9RQ57 buchnera ap |
| 31 | 12 | 27.9 | 8 | 4 Q81VK3 | Q81VK3 homo sapien |
| 32 | 12 | 27.9 | 8 | 6 Q9GMH3 | Q9GMH3 lagenorhync |
| 33 | 12 | 27.9 | 8 | 6 Q28866 | Q28866 megaptera n |
| 34 | 12 | 27.9 | 8 | 8 Q19961 | Q19961 gossypium d |
| 35 | 12 | 27.9 | 8 | 8 Q19958 | Q19958 gossypium b |
| 36 | 12 | 27.9 | 8 | 8 Q94V82 | Q94V82 varanus yuw |
| 37 | 12 | 27.9 | 8 | 8 Q19960 | Q19960 gossypium m |
| 38 | 12 | 27.9 | 8 | 8 Q19959 | Q19959 gossypium t |
| 39 | 12 | 27.9 | 8 | 8 Q19956 | Q19956 gossypium a |
| 40 | 12 | 27.9 | 8 | 10 Q8GTG5 | Q8GTG5 lycopersico |
| 41 | 11 | 25.6 | 7 | 5 Q7Z1C0 | Q7Z1C0 caenorhabdi |
| 42 | 11 | 25.6 | 7 | 15 Q8JE81 | Q8JE81 human immun |
| 43 | 11 | 25.6 | 8 | 2 Q9RQ43 | Q9RQ43 buchnera ap |
| 44 | 11 | 25.6 | 8 | 2 Q09258 | Q09258 synechococc |
| 45 | 11 | 25.6 | 8 | 2 Q9ZIE9 | Q9ZIE9 neisseria m |

ALIGNMENTS

RESULT 1

P92214 ID P92214 PRELIMINARY; PRT; 7 AA.
AC P92214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein l1 (Fragment).
GN RPS11.
OS Amblyopyrum muticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL EMBL; Z77756; CAB01346.1; -.
DR Mol. Phylogenet. Evol. 7:217-230(1997).
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4

DB 1 PPK 3

RESULT 2

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P92393
ID P92393 PRELIMINARY; PRT; 7 AA.
AC P92393
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H3139; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77764; CAB01370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

RESULT 3
P92403 PRELIMINARY; PRT; 7 AA.
ID P92403
AC P92403
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Lophopyrum elongatum (Tall wheatgrass) (Aegilops elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6692; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01307.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

P92403 PRELIMINARY; PRT; 7 AA.
ID P92403
AC P92403
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

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RESULT 4
P92427 PRELIMINARY; PRT; 7 AA.
ID P92427
AC P92427
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01325.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

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RESULT 5
P92430 PRELIMINARY; PRT; 7 AA.
ID P92430
AC P92430
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

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Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

RESULT 6
P22221 ID P22221 PRELIMINARY; PRT; 7 AA.
AC P22221;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromaeae; Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

RESULT 7
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AC P2425;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Qy      2 PPR 4
Db      1 PPK 3

RESULT 8
P2381 ID P2381 PRELIMINARY; PRT; 7 AA.
AC P2381;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

RESULT 9
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AC P2387;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

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SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 10
P92210 PRELIMINARY; PRT; 7 AA.
ID P92210;
AC P92210;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum (Crested wheatgrass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77771; CAB01391.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 11
P92440 PRELIMINARY; PRT; 7 AA.
ID P92440;
AC P92440;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77769; CAB01385.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 12
P92218 PRELIMINARY; PRT; 7 AA.
ID P92218;
AC P92218;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77767; CAB01379.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 13
P92390 PRELIMINARY; PRT; 7 AA.
ID P92390;
AC P92390;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Heteranthelium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Heteranthelium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";

```

```

RT sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01328.1; -.
KW GO; GO:0009507; C:chloroplast; IEA.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match
Best Local Similarity 37.2%; Score 16; DB 8; Length 7;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

RESULT 14
P92372 PRELIMINARY; PRT; 7 AA.
AC P92372;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Haynaldia villosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.
OX NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
KW GO; GO:0009507; C:chloroplast; IEA.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match
Best Local Similarity 37.2%; Score 16; DB 8; Length 7;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

RESULT 15
P92442 PRELIMINARY; PRT; 7 AA.
AC P92442;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Taeniatherum caput-medusae (Medusahead).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;

```

```

RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01358.1; -.
KW GO; GO:0009507; C:chloroplast; IEA.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match
Best Local Similarity 37.2%; Score 16; DB 8; Length 7;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

Search completed: July 28, 2004, 07:54:56
Job time : 35 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:15:39 ; Search time 50 seconds
(without alignments)
45.208 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 43 | 100.0 | 8 | 3 AAB19055 | Aab19055 Amino aci |
| 2 | 38 | 88.4 | 8 | 2 AAY28537 | Aay28537 Beta-1 in |
| 3 | 36 | 83.7 | 8 | 2 AAU06877 | Aau06877 Glycosami |
| 4 | 33 | 76.7 | 7 | 2 AAY28538 | Aay28538 Beta-1 in |
| 5 | 31 | 72.1 | 8 | 2 AAR59381 | Aar59381 Fibronect |
| 6 | 31 | 72.1 | 8 | 2 AAR56244 | Aar56244 Fibronect |
| 7 | 31 | 72.1 | 8 | 2 AAY78582 | Aay78582 Fibronect |
| 8 | 31 | 72.1 | 8 | 2 AAR83682 | Aar83682 33 kD fib |
| 9 | 31 | 72.1 | 8 | 2 AAU46437 | Aau46437 Synthetic |
| 10 | 31 | 72.1 | 8 | 2 AAU19843 | Aau19843 Chimeric |
| 11 | 31 | 72.1 | 8 | 2 AAW73537 | Aaw73537 Fibronect |
| 12 | 31 | 72.1 | 8 | 2 AAW81843 | Aaw81843 Fibronect |
| 13 | 31 | 72.1 | 8 | 2 AAY32881 | Aay32881 Fibronect |
| 14 | 31 | 72.1 | 8 | 2 AAY32869 | Aay32869 Fibronect |
| 15 | 31 | 72.1 | 8 | 2 AAY28545 | Aay28545 Beta-1 in |
| 16 | 31 | 72.1 | 8 | 4 AAB91965 | Aab91965 Fibronect |
| 17 | 31 | 72.1 | 8 | 4 AAB91982 | Aab91982 Fibronect |
| 18 | 28 | 65.1 | 6 | 2 AAR62181 | Aar62181 UL snRNP |
| 19 | 28 | 65.1 | 7 | 2 AAR73883 | Aar73883 Rubella v |
| 20 | 26 | 60.5 | 6 | 2 AAY28511 | Aay28511 Beta-1 in |
| 21 | 26 | 60.5 | 6 | 3 AAB19065 | Aab19065 Amino aci |
| 22 | 25 | 58.1 | 7 | 2 AAR73902 | Aar73902 Streptoco |
| 23 | 25 | 58.1 | 7 | 7 ADC44364 | Adc44364 Endotheli |
| 24 | 25 | 58.1 | 8 | 2 AAY40669 | Aay40669 A2 deriva |
| 25 | 25 | 58.1 | 8 | 3 AAB30008 | Aab30008 Scaffold |

| | | | | | |
|----|----|------|---|------------|--------------------|
| 26 | 24 | 55.8 | 7 | 2 AAR73879 | Aar73879 Rubella v |
| 27 | 24 | 55.8 | 7 | 4 AAG98209 | Aag98209 Human SNP |
| 28 | 23 | 53.5 | 7 | 2 AAR09404 | Aar09404 LFA-1 alp |
| 29 | 22 | 53.5 | 7 | 7 ADC28167 | Adc28167 Synthetic |
| 30 | 22 | 51.2 | 7 | 2 AAW34386 | Aaw34386 PKB subst |
| 31 | 22 | 51.2 | 7 | 2 AAW71730 | Aaw71730 Peptide # |
| 32 | 22 | 51.2 | 7 | 3 AAY95265 | Aay95265 Crostide |
| 33 | 22 | 51.2 | 7 | 4 AAB99790 | Aab99790 Protein k |
| 34 | 22 | 51.2 | 7 | 4 AAG65169 | Aag65169 AKT inhib |
| 35 | 22 | 51.2 | 7 | 4 AAB83202 | Aab83202 PKA inhib |
| 36 | 22 | 51.2 | 7 | 4 AAB59271 | Aab59271 Phosphory |
| 37 | 22 | 51.2 | 7 | 5 AAG66179 | Aag66179 Peptide s |
| 38 | 22 | 51.2 | 7 | 5 AAO19502 | Aao19502 AKT inhib |
| 39 | 22 | 51.2 | 7 | 6 ABU08523 | Abu08523 Protein k |
| 40 | 22 | 51.2 | 7 | 7 ADC81657 | Adc81657 Protein k |
| 41 | 22 | 51.2 | 7 | 7 ADE49662 | Ade49662 Pyrazole |
| 42 | 22 | 51.2 | 8 | 2 AAR32362 | Aar32362 Sample pe |
| 43 | 22 | 51.2 | 8 | 2 ABB76926 | Abb76926 Cyclohex |
| 44 | 22 | 51.2 | 8 | 2 AAY33180 | Aay33180 Human pef |
| 45 | 22 | 51.2 | 8 | 2 AAY48023 | Aay48023 Immunogen |

ALIGNMENTS

RESULT 1

AAB19055

ID AAB19055 standard; peptide; 8 AA.

XX

AC AAB19055;

XX

DT 08-FEB-2001 (first entry)

XX

DE Amino acid sequence of a betal-integrin inhibitor.

XX

KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;

KW Central nervous system ischemic injury; myocardial infarction;

KW Betal-integrin; angioplasty; surgical incision; injury-related trauma;

KW Transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.

OS Synthetic.

XX

XX WO200056350-A2.

XX

PD 28-SEP-2000.

XX

PF 22-MAR-2000; 2000WO-US007680.

XX

PR 22-MAR-1999; 99US-0125634P.

PR 24-NOV-1999; 99US-0167538P.

PA

(MINU) UNIV MINNESOTA.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (SENT-) SENTRON MEDICAL INC.

XX

PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;

PI Furcht LT;

XX

DR WPI; 2000-656062/63.

XX

PT Inhibition of inflammatory leukocyte mediated destruction of tissue in a patient, comprises administering a peptide inhibitor of betal-integrin, useful for treatment of e.g. cancer and osteoporosis.

XX

PS Claim 3; Page 38; 61pp; English.

XX

CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit betal-integrin which is responsible for leukocyte mediated tissue destruction. The peptides are useful for inhibiting inflammatory

CC leukocyte mediated destruction of tissue which occurs as a result of

CC central nervous system (CNS) ischemic injury, myocardial infarction, angioplasty, surgical incisions, injury-related trauma, and/or transplant

CC reperfusion, exposure to heat, cold, light, electricity and/or chemicals.

CC They are also useful for the treatment of stroke, a burn type injury,
 XX cancer, and osteoporosis

SQ Sequence 8 AA;

Query Match 100.0%; Score 43; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRAAIY 8
 |||||

DB 1 QPPRAAIY 8

RESULT 2

AAAY28537
 ID AAY28537 standard; peptide; 8 AA.

XX AC AAY28537;

XX DT 19-OCT-1999 (first entry)

XX DE Beta-1 integrin cell adhesion modulator analogue #22.

XX KW Beta 1 integrin dependent cell adhesion; lipAr motif; tumour;

XX KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.

XX OS Synthetic.

XX FN WO9937669-A1.

XX PD 29-JUL-1999.

XX PF 21-JAN-1999; 99WO-US001236.

XX PR 22-JAN-1998; 98US-00721119P.

XX PR 12-AUG-1998; 98US-0096211P.

XX PR 12-AUG-1998; 98US-0096212P.

XX PA (MINU) UNIV MINNESOTA.

XX PI McCarthy JB, Furcht LT, Brienza A;

XX DR WPI; 1999-469112/39.

XX PT New peptides modulating beta1 integrin subunit dependent cell adhesion,
 PT useful to study cell adhesion e.g. alpha4beta1 integrin dependent
 PT adhesion important in tumor cell biology.

XX PS Example 4; Fig 7; 47pp; English.

XX CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which has
 CC a side chain including an aromatic group, and a penultimate C-terminal
 CC amino acid residue (Lip) with an alkyl side chain group, i.e. a 'LipAr'
 CC motif. Studies with these peptides have also shown that inhibiting
 CC peptides do not contain D-amino acids and that it is the presence of the
 CC ArLip motif that conveys effective beta1 integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer

XX SQ Sequence 8 AA;

Query Match 88.4%; Score 38; DB 2; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAIY 8
 |||||

DB 1 QPPRAIY 8

RESULT 3

AAW06877
 ID AAW06877 standard; peptide; 8 AA.

XX AC AAW06877;

XX DT 18-MAR-1997 (first entry)

XX DE Glycosaminoglycan binding peptide from fibronectin.

XX KW Complement inhibitor; membrane co-factor protein; MCP;
 KW decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
 KW heparin; cell lysis; sepsis; adult respiratory distress syndrome;
 KW reperfusion injury; cell damage; therapy; fibronectin.

XX OS Synthetic.

XX PN WO9634965-A2.

XX PD 07-NOV-1996.

XX PF 03-MAY-1996; 96WO-US006301.

XX PR 05-MAY-1995; 95US-00435149.

XX PA (CHTR) CHIRON CORP.

XX PI Innis MA, Zaror I, Creasey AA;

XX DR WPI; 1996-506167/50.

XX CC Chimeric proteins for inhibiting complement-mediated cell lysis -
 PT comprise membrane co-factor protein and decay accelerating factor peptide
 PT sequences.

XX PS Claim 9; Page 26; 33pp; English.

XX CC A glycosaminoglycan binding peptide (AAW06877) derived from fibronectin
 CC is utilised in novel chimeric proteins of the formula A-R1-B-R2-C, where
 CC A and C are peptides (AAW06875-79, AAW06883-90) capable of binding
 CC glycosaminoglycans (esp. heparin), present on cell surfaces. R1 is
 CC membrane co-factor protein (MCP) or decay accelerating factor (DAF), R2
 CC is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may
 CC have complement inhibitor activity. The chimeric proteins (see also
 CC AAW06882) are directed to cell surfaces where they inhibit complement-
 CC mediated cell lysis. They are used to treat and prevent disease states in
 CC which complement plays a role, e.g. sepsis, adult respiratory distress
 CC syndrome, reperfusion injury and tissue damage

XX SQ Sequence 8 AA;

Query Match 83.7%; Score 36; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||

DB 2 QPPRAAI 8

RESULT 4

AAAY28538
 ID AAY28538 standard; peptide; 7 AA.

XX AC AAY28538;

XX DT 19-OCT-1999 (first entry)

XX DE Beta-1 integrin cell adhesion modulator analogue #23.

KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 OS Synthetic.

XX WO9937669-A1.
 XX
 XX 29-JUL-1999.

XX
 XX 21-JAN-1999; 99WO-US001236.
 XX
 XX 22-JAN-1998; 98US-0072119P.
 PR 12-AUG-1998; 98US-0096211P.
 PR 12-AUG-1998; 98US-0096212P.

XX (MINU) UNIV MINNESOTA.

XX McCarthy JB, Furcht LT, Brienza A;
 XX WPI; 1998-469112/39.

XX New peptides modulating betal integrin subunit dependent cell adhesion,
 PT useful to study cell adhesion e.g. alpha4betal integrin dependent
 PT adhesion important in tumor cell biology.

XX Example 4; Fig 7; 47pp; English.

XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AA28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which has
 CC a side chain including an aromatic group, and a penultimate C-terminal
 CC amino acid residue (Lip) with an alkyl side chain group, i.e. a 'LipAr'
 CC motif. Studies with these peptides have also shown that inhibiting
 CC peptides do not contain D-amino acids and that it is the presence of the
 CC Arlip motif that conveys effective betal integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer
 XX

XX Sequence 7 AA;

Query Match 76.7%; Score 33; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PPRAAIY 8
 DB 1 PPRARIY 7

RESULT 5
 AAR59381
 ID AAR59381 standard; peptide; 8 AA.

XX AAR59381;
 XX
 XX 25-MAR-2003 (revised)
 DT 22-MAR-1995 (first entry)
 XX
 XX Fibronectin fragment FN5.

XX Fibronectin; retro virus; HIV; AIDS; virucide; ovalbumin.
 XX Synthetic.

XX WO9417097-A1.
 XX
 XX 04-AUG-1994.

XX 19-JAN-1994; 94WO-US000729.

XX

PR 19-JAN-1993; 93US-00006121.
 XX (MINU) UNIV MINNESOTA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wahl SM, McCarthy JB, Furcht LT;
 XX WPI; 1994-264029/32.

XX New polypeptide comprising carrier molecule coupled to fibronectin
 PT fragment - useful in treatment of retroviral infections and associated
 PT diseases, e.g. AIDS.

XX Claim 1; Page 13; 18pp; English.

XX This peptide may be covalently linked to a carrier (especially
 CC ovalbumin). The resulting compound FN-C/H-V has excellent HIV virus
 CC inhibiting activity, low toxicity and high safety. It may be useful in
 CC the treatment of AIDS. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QPPRAAI 7
 DB 2 QPPRARI 8

RESULT 6
 AAR56244
 ID AAR56244 standard; peptide; 8 AA.

XX AAR56244;

XX 25-MAR-2003 (revised)

DT 12-JAN-1995 (first entry)

XX Fibronectin-derived peptide.

XX Fibronectin; inflammation; antiinflammatory; immunosuppressive;
 KW leukocyte; arthritis; autoimmune disease; graft versus host disease.

XX Synthetic.

XX WO9413692-A1.

XX 23-JUN-1994.

XX 06-DEC-1993; 93WO-US011781.

XX 10-DEC-1992; 92US-00990296.

PR 21-OCT-1993; 93US-00139903.

XX (MINU) UNIV MINNESOTA.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Furcht JT, McCarthy JB, Wahl SM, Allen JB;

XX WPI; 1994-217799/26.

XX Fibronectin derived peptide(s) for treating inflammation - involving
 PT leukocyte activation, partic. arthritis and graft versus host disease.

XX Claim 8; Page 31; 45pp; English.

XX Chronic inflammation or autoimmune diseases are treated with peptides
 CC corresponding to residues 1906-24 (AAR56242), 1946-60 (AAR56243), 1892-99
 CC (AAR56244), 1961-85 (AAR56245), 1784-92 (AAR56246) and 1485-504
 CC (AAR56247) of fibronectin. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 8 AA;
 Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QPPRAAI 7
 |||||
 Db 2 QPPRARI 8
 RESULT 7
 AAY78582
 ID AAY78582 standard; peptide; 8 AA.
 XX
 AC AAY78582;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Fibronectin derived peptide FN-C/H-V.
 XX
 KW Fibronectin; intraocular fibroblast proliferation inhibitor; glaucoma;
 KW proliferative retinopathy; fibroblast migration; scarring.
 XX
 OS Unidentified.
 XX
 PN US6013628-A.
 XX
 PD 11-JAN-2000.
 XX
 XX 27-FEB-1995; 95US-00394748.
 XX
 PR 28-FEB-1994; 94US-00203458.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Gregerson DS, Agarwal A, Wright MM, Murali S, Skubitz APN;
 PI Furcht LT, Balles M;
 XX
 DR WPI; 1995-320291/41.
 XX
 XX Treating proliferative vitreo:retinopathy, retinal scarring and glaucoma
 PT - using peptide derived from fibronectin, laminin or collagen.
 XX
 PS Example 1; Col 15; 44pp; English.
 XX
 CC This sequence represents a fibronectin derived peptide. Ocular
 CC administration of the peptide inhibits fibroblast proliferation and can
 CC be used in the treatment of glaucoma. The peptide can be used to treat
 CC proliferative vitreo:retinopathy by ocular administration of the peptides
 CC of the invention, which suppress fibroblast-mediated collagen gel
 CC contraction. The peptides can be used for treating glaucoma in mammals,
 CC especially humans, by inhibiting intraocular fibroblast proliferation,
 CC fibroblast migration and scarring
 XX
 SQ Sequence 8 AA;
 Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QPPRAAI 7
 |||||
 Db 2 QPPRARI 8
 RESULT 8
 AAR83682
 ID AAR83682 standard; peptide; 8 AA.
 XX
 AC AAR83682;
 XX
 DT 25-MAR-2003 (revised)

DT 11-APR-1996 (first entry)
 XX
 DE 33 kD fibronectin A chain peptide FN-C/H-V (1892-1899).
 XX
 KW 33 kD fragment; A chain; fibronectin; fibroblast; cell; proliferation;
 KW supression; epithelial; glial; epiretinal; eye; membranes; contraction;
 KW migration; vitreo:retinopathy; scarring; vitreo:retinal; glaucoma.
 XX
 OS Synthetic.
 XX
 PN WO9522979-A1.
 XX
 PD 31-AUG-1995.
 XX
 PF 28-FEB-1995; 95WO-US002478.
 XX
 PR 28-FEB-1994; 94US-00203458.
 PR 27-FEB-1995; 95US-00394748.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Skubitz AP, Furcht LT, Balles M, Gregerson DS, Agarwal A;
 PI Wright MM, Murali S;
 XX
 DR WPI; 1995-320291/41.
 XX
 XX Treating proliferative vitreo:retinopathy, retinal scarring and glaucoma
 PT - using peptide derived from fibronectin, laminin or collagen.
 XX
 PS Example 1; Page 29; 84pp; English.
 XX
 CC A polypeptide which includes at least five amino acids from a fragment of
 CC the fibronectin A chain (AAR83679-84), C-terminal G domain of the laminin
 CC A chain (AAR83642/78) or N1 domain of the alpha-2 chain of type IV
 CC collagen (AAR83639-41) suppresses fibroblast, epithelial and glial cell
 CC proliferation, contraction of epiretinal membranes and cell migration
 CC within the eye. It may be used in the treatment of proliferative
 CC vitreo:retinopathy, vitreo:retinal scarring and glaucoma. (Updated on 25-
 CC MAR-2003 to correct PR field.)
 XX
 SQ Sequence 8 AA;
 Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QPPRAAI 7
 |||||
 Db 2 QPPRARI 8
 RESULT 9
 AAW46437
 ID AAW46437 standard; peptide; 8 AA.
 XX
 AC AAW46437;
 XX
 DT 14-MAY-1998 (first entry)
 XX
 DE Synthetic peptide Pn5 which binds pneumococci.
 XX
 KW fibronectin; adherence; vaccine; antibody passive immunisation;
 KW diagnosis; screening; treatment; prevention; bacterial infection.
 XX
 OS Synthetic.
 XX
 PN WO9741151-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97WO-US007198.
 XX
 PR 01-MAY-1996; 96US-0016632P.

```

PR 01-MAY-1996; 96US-00642250.
XX (UTRQ ) UNIV ROCKEFELLER.
PA Masure HR, Rosenow CI, Tuomanen E, Wizeman TM;
PI WPI; 1997-549682/50.
XX
XX New isolated streptococcal choline binding proteins - used to develop
PT products for treating or preventing bacterial infection and for
PT detection, diagnosis and screening.
XX
XX Claim 34; Page 14; 142pp; English.
PS
CC The present sequence represents a synthetic peptide, Fn5. Streptococcus
CC pneumoniae (pneumococci) adheres to fibronectin at a site within the
CC carboxy-terminal heparin II binding domain. An eight amino acid stretch
CC within the type III #14 repeat supports adherence. The present peptide is
CC based on these amino acids. S. pneumoniae binds directly to this peptide.
CC An antibody to Fn5 inhibits adherence of S. pneumoniae to whole
CC fibronectin by greater than 70%. The peptide can be used to prepare
CC vaccines. The antibodies can be used for passive immunisation,
CC diagnostics, or screening. The peptide can also be used for treating or
CC preventing bacterial infection
XX
XX Sequence 8 AA;
SQ
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db |||||
2 QPPRAAI 8

RESULT 10
AAW19843
ID AAW19843 standard; peptide; 8 AA.
XX
XX AAW19843;
AC
XX 26-JAN-1998 (first entry)
DT
XX Chimeric adenovirus coat protein heparin binding motif.
DE
XX Adenovirus; vector; coat protein; Gene therapy; gene transfer; human;
KW cancer; autoimmune disease; heart disease; infection; heparin.
KW
XX Synthetic.
XX
XX WO9720051-A2.
FN
XX 05-JUN-1997.
PD
XX 27-NOV-1996; 96WO-US019150.
XX
XX 28-NOV-1995; 95US-00563368.
PR
XX 21-AUG-1996; 96US-00700846.
PR
XX 21-AUG-1996; 96US-00701124.
XX
XX (GENV-) GENVEC INC.
PA
XX Wickham TJ, Kovessdi I, Brough DE;
PI
XX WPI; 1997-310606/28.
XX
XX Adenoviral vectors containing chimeric coat protein - bind and enter
PT cells more efficiently, useful for gene therapy of e.g. cancer,
PT auto-immune diseases, etc.
XX
XX Claim 7; Page 19; 121pp; English.
XX

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CC This peptide is used as a universal transfer vector (UTV) sequence or as
CC a spacer sequence in novel chimeric adenovirus coat proteins (CP),
CC especially chimeric fibre proteins. It comprises a heparin binding motif
CC derived from fibronectin. Claimed UTVs/spacers are given in AAW19810-11,
CC AAW19813-25, AAW19827, AAW19829, AAW19831-32 and AAW19834-43. Claimed
CC chimeric CPs differ from the wild-type CP by the introduction of the UTV
CC and/or spacer at or near the C-terminus or in an exposed loop. This
CC imparts on the chimeric CP the ability to bind to and enter cells by
CC means of a novel cell surface binding site. Recombinant vectors
CC comprising the chimeric CP are able to enter cells more efficiently than
CC vectors comprising wild-type CP, especially at lower m.o.i. They are
CC especially useful for gene therapy of e.g. cancers, genetic disorders,
CC pathogenic infections, heart disease or autoimmune diseases
XX
XX Sequence 8 AA;
SQ
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db |||||
2 QPPRAAI 8

RESULT 11
AAW73537
ID AAW73537 standard; peptide; 8 AA.
XX
XX AAW73537;
AC
XX 04-MAR-1999 (first entry)
DT
XX Fibronectin fragment, peptide FN-C/H-V.
DE
XX Adhesion promoter; extra-cellular matrix peptide;
KW biomolecule immobilisation; fibronectin.
XX
XX Synthetic.
XX
XX US5853744-A.
PN
XX 29-DEC-1998.
FD
XX
XX 20-AUG-1996; 96US-00699965.
XX
XX 20-AUG-1996; 96US-00699965.
PR
XX (MINU ) UNIV MINNESOTA.
XX
XX Mooradian DL, Fields GB;
PI
XX WPI; 1999-094819/08.
XX
XX Solid-phase method for modifying substrate with peptide, especially
PT adhesion-promoting peptide - applied to medical devices, e.g. vascular
PT grafts, uses peptide modified by photoreactive group for covalent
PT attachment.
XX
XX Claim 4; Fig 1; 14pp; English.
PS
XX
XX This sequence represents a fragment of fibronectin, and is designated
CC peptide FN-C/H-V. This sequence is an adhesion promoting extra-cellular
CC matrix peptide, and can be used in the method of the invention. The
CC method is a solid-phase method for modifying a substrate surface to
CC include a biomolecule (I), and comprises: (a) providing an immobilised
CC (I), comprising a peptide having: (i) an N alpha-terminus; or (ii) an
CC active site, by covalently attaching it to a support; (b) attaching a
CC photoreactive crosslinking agent (II), having at least one photoreactive
CC group, to the immobilised peptide, in (i) at the N alpha-terminus or in
CC (ii) to the peptide at an amino acid that does not form part of the
CC active site; (c) removing the photoreactive analogue (Ia) of (I) from the
CC support; and (d) attaching (Ia) to a solid surface by activating the
CC

```

CC photoreactive group. The method is particularly used to immobilise (I) on
 CC medical devices, specifically adhesion-promoting peptides on vascular
 CC grafts such that adhesion of cells to the device is improved. More
 CC generally a wide range of peptides can be deposited on blood oxygenators,
 CC pumps or sensors; tubing; stents; pacemaker leads; heart valves; (I)
 CC catheters; artificial organs; or body implants generally. Bound (I)
 CC retains its native activity, specifically promotion of adhesion and
 CC spreading of vascular endothelial cells. The method ensures that (II)
 CC reacts with alpha-amino groups only (contrast use of soluble peptide
 CC where reaction may occur at epsilon-amino groups in the active site) and
 CC a large excess of (II) can be used to avoid wasting peptide
 XX
 XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||
 DB 2 QPPRARI 8

RESULT 12
 ID AAW81843 standard; peptide; 8 AA.

XX AAW81843;

DT 17-OCT-2003 (revised)
 DT 05-FEB-1999 (first entry)

XX Fibronectin-like peptide V.

XX Fibronectin; ischemia; treatment; inflammatory disease; A chain;
 KW heparin-binding; RGDS-mediated cell adhesion region.

XX unidentified.

XX US5840691-A.

XX 24-NOV-1998.

XX 07-JUN-1995; 95US-00480133.

XX 10-DEC-1992; 92US-00990296.

XX 21-OCT-1993; 93US-00139903.

XX (FURC/) FURCHT L T.

XX (WAHL/) WAHL S M.

XX (ALLE/) ALLEN J B.

XX (BILL/) BILLUPS K L.

XX (MCCA/) MCCARTHY J B.

XX (EVER/) EVERETT J E.

XX Allen JB, Wahl SM, Everett JE, McCarthy JB, Furcht LT;
 PI Billups KL;

XX WPI; 1999-034077/03.

XX Treatment of ischaemia - with fibronectin peptides.

XX Claim 1; Col 25-26; 35pp; English.

XX AAW81841-W81846 are peptides used in a method for treating ischemia using
 CC polypeptides with fibronectin activity. The method can be used for
 CC treating a number of disease such as those associated with inflammatory
 CC diseases by administering an effective amount of a composition containing
 CC a polypeptide having a sequence of at least 3 amino acids corresponding
 CC substantially to an amino acid sequence within the 33 kd carboxyl
 CC terminal heparin-binding region located on the A chain of fibronectin or
 CC an RGDS-containing amino acid sequence within the 11.5 kd RGDS-mediated
 CC cell adhesion region located on all isoforms of fibronectin. (Updated on

CC 17-OCT-2003 to standardise OS field)
 XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||
 DB 2 QPPRARI 8

RESULT 13

AAAY32881

ID AAY32881 standard; peptide; 8 AA.

XX AAY32881;

DT 02-NOV-1999 (first entry)

DE Fibronectin protein heparin II binding domain peptide H-V.

XX Fibronectin; extracellular matrix. open wound healing; IIICS domain;

KW acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;

XX wound healing promoter; cell binding domain; heparin II binding domain.

OS Homo sapiens.

XX WO9942117-A1.

XX 26-AUG-1999.

XX 10-FEB-1999; 99WO-US002872.

XX 18-FEB-1999; 98US-00025622.

XX (UYNV) UNIV NEW YORK STATE RES FOUND.

XX Clark RA, Greiling D;

XX WPI; 1999-527415/44.

XX New extracellular matrix used to accelerate healing of acute gaping
 PT cutaneous wounds and chronic cutaneous ulcers.

XX Claim 14; Page 19; 43pp; English.

XX This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix of the invention. The extracellular matrix comprises
 CC two or more fibronectin domains in a backbone matrix, and is used to
 CC enhance wound healing. The fibronectin domain peptides used are
 CC preferably from the IIICS domain, the cell binding domain, or the heparin
 CC II binding domain of human fibronectin. The matrix facilitates wound
 CC healing by providing an environment that intrinsically recruits new
 CC tissue cells to the wound site. The new matrix is useful for facilitating
 CC wound healing, especially useful for treating open wounds such as acute
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of
 CC chronic, non-healing wounds is severe. These open wounds require long-
 CC term care and procedures that are costly and labour intensive.
 CC Furthermore, these wounds have a severe impact on the patients' quality of
 CC life. Prior compositions and matrices have not been useful or cost
 CC effective. The present invention provides a matrix for wound healing that
 CC meets these requirements, and overcomes the deficiencies of the prior
 CC matrices

XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

```

Db      2 QPPRAI 8
|||||
RESULT 14
AAY32869
ID AAY32869 standard; peptide; 8 AA.
XX
AC AAY32869;
XX
DT 02-NOV-1999 (first entry)
XX
DE Fibronectin protein heparin II binding domain peptide H-V.
XX
KW Fibronectin; extracellular matrix; wound healing promoter; IIICS domain;
KW cell binding domain; heparin II binding domain; haemostasis; therapy;
KW surgical incisional wound; traumatic wound; radiation wound;
KW cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.
XX
OS Homo sapiens.
XX
PN WO9942126-A1.
XX
PD 26-AUG-1999.
XX
PF 10-FEB-1999; 99WO-US002873.
XX
PR 18-FEB-1998; 98US-00025706.
XX
PA (UNYU ) UNIV NEW YORK STATE RES FOUND.
XX
PI Clark RA, Greiling D, Gaillit J;
XX
DR WPI; 1999-527421/44.
XX
PT Extracellular matrix for promoting wound healing containing recombinant
PT fibronectin-derived peptide and backbone matrix.
XX
PS Claim 14; Page 21; 48pp; English.
XX
CC This sequence represents a fibronectin protein fragment used in the
CC extracellular matrix (A) of the invention. (A) is used for promoting
CC wound healing, and comprises a recombinant fibronectin peptide,
CC containing peptide fragments from at least two fibronectin domains, and a
CC backbone matrix. The fibronectin domain peptides used are preferably from
CC the IIICS domain, the cell binding domain, or the heparin II binding
CC domain of human fibronectin. (A) provides haemostasis and an environment
CC that recruits new tissue cells to the site of the wound. (A) is used to
CC promote healing of acute or chronic wounds, e.g. surgical incisional
CC wounds, traumatic wounds, radiation wounds, cancer extirpations, venous
CC leg ulcers, diabetic ulcers and pressure ulcers
XX
SQ Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8
|||||

RESULT 15
AAY28545
ID AAY28545 standard; peptide; 8 AA.
XX
AC AAY28545;
XX
DT 19-OCT-1999 (first entry)
XX
DE Beta-1 integrin cell adhesion modulator analogue #37.
XX
KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
OS Synthetic.
XX
PN WO9937669-A1.
XX
PD 29-JUL-1999.
XX
PF 21-JAN-1999; 99WO-US001236.
XX
PR 22-JAN-1998; 98US-0072119P.
PR 12-AUG-1998; 98US-0096211P.
PR 12-AUG-1998; 98US-0096212P.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI McCarthy JB, Furcht LT, Brienza A;
XX
DR WPI; 1999-469112/39.
XX
PT New peptides modulating betal integrin subunit dependent cell adhesion,
PT useful to study cell adhesion e.g. alpha4beta1 integrin dependent
PT adhesion important in tumor cell biology.
XX
PS Example 8; Fig 13; 47pp; English.
XX
CC This peptide is used with AAY28510-Y28549 to show that peptides which
CC modulate beta-1 integrin subunit dependent cell adhesion need a C-
CC terminal amino acid residue (Ar) which has a side chain including an
CC aromatic group. They also need a penultimate C-terminal amino acid
CC residue (Lip) with an alkyl side chain group, i.e. a 'LipAr' motif.
CC Studies with these peptides have also shown that inhibiting peptides do
CC not contain D-amino acids and that it is the presence of the ArLip motif
CC that conveys effective betal integrin dependent cell adhesion inhibition.
CC The beta-1 integrin subunit dependent cell adhesion is important for cell
CC adhesion to extracellular matrix proteins, and the subunit is expressed
CC on tumours such as melanomas. Therefore these LipAr motif containing
CC peptides may be important in the treatment of cancer
XX
SQ Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8
|||||

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Job time : 52 secs

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Run on: July 28, 2004, 07:55:00 ; Search time 41 Seconds
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Title: SFQ3

Perfect score: 43
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Scoring table: BLOSUM62
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Searched: 1291335 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 67706

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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 31 | 72.1 | 8 | 9 | US-09-765-614B-6 |
| 2 | 31 | 72.1 | 8 | 9 | US-09-925-715-2 |
| 3 | 31 | 72.1 | 8 | 10 | US-09-999-724-58 |
| 4 | 31 | 72.1 | 8 | 10 | US-09-829-382-11 |
| 5 | 31 | 72.1 | 8 | 14 | US-10-017-193-4 |
| 6 | 31 | 72.1 | 8 | 16 | US-10-722-075-6 |
| 7 | 28 | 65.1 | 8 | 9 | US-09-765-614B-3 |
| 8 | 28 | 65.1 | 8 | 16 | US-10-722-075-3 |
| 9 | 25 | 58.1 | 7 | 14 | US-10-286-457-92 |
| 10 | 24 | 55.8 | 7 | 16 | US-10-346-737A-6 |
| 11 | 23 | 53.5 | 7 | 10 | US-09-954-385-360 |
| 12 | 23 | 53.5 | 7 | 14 | US-10-021-660-90 |
| 13 | 22 | 51.2 | 7 | 9 | US-09-845-667-6 |
| 14 | 22 | 51.2 | 7 | 9 | US-09-845-667-21 |
| 15 | 22 | 51.2 | 7 | 9 | US-09-845-667-56 |

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|----|------|---|----|--------------------|--------------------|
| 16 | 51.2 | 7 | 14 | US-10-190-012-9 | Sequence 9, Appli |
| 17 | 51.2 | 7 | 14 | US-10-148-786A-15 | Sequence 15, Appli |
| 18 | 51.2 | 8 | 9 | US-09-245-764-4 | Sequence 4, Appli |
| 19 | 51.2 | 8 | 12 | US-10-687-109-4 | Sequence 4, Appli |
| 20 | 48.8 | 7 | 9 | US-09-845-667-13 | Sequence 13, Appli |
| 21 | 48.8 | 7 | 10 | US-09-931-325A-120 | Sequence 120, App |
| 22 | 48.8 | 7 | 10 | US-09-931-325A-124 | Sequence 124, App |
| 23 | 48.8 | 7 | 10 | US-09-954-385-414 | Sequence 114, App |
| 24 | 48.8 | 7 | 10 | US-09-930-915A-160 | Sequence 160, App |
| 25 | 48.8 | 7 | 10 | US-09-930-915A-165 | Sequence 165, App |
| 26 | 48.8 | 8 | 8 | US-08-344-824-263 | Sequence 263, App |
| 27 | 48.8 | 8 | 9 | US-09-839-666-6 | Sequence 6, Appli |
| 28 | 48.8 | 8 | 10 | US-09-931-325A-122 | Sequence 122, App |
| 29 | 48.8 | 8 | 10 | US-09-930-915A-163 | Sequence 163, App |
| 30 | 48.8 | 8 | 12 | US-10-372-735-65 | Sequence 65, Appli |
| 31 | 48.8 | 8 | 12 | US-10-029-926B-14 | Sequence 14, Appli |
| 32 | 48.8 | 8 | 14 | US-10-234-579-6 | Sequence 6, Appli |
| 33 | 48.8 | 8 | 15 | US-10-032-017B-14 | Sequence 14, Appli |
| 34 | 48.8 | 8 | 15 | US-10-029-988B-14 | Sequence 14, Appli |
| 35 | 48.8 | 8 | 15 | US-10-032-423A-14 | Sequence 14, Appli |
| 36 | 46.5 | 4 | 9 | US-09-802-077-59 | Sequence 59, Appli |
| 37 | 46.5 | 4 | 9 | US-09-802-096-59 | Sequence 59, Appli |
| 38 | 46.5 | 4 | 9 | US-09-871-974-12 | Sequence 12, Appli |
| 39 | 46.5 | 4 | 10 | US-09-925-179-59 | Sequence 59, Appli |
| 40 | 46.5 | 4 | 15 | US-10-137-867-186 | Sequence 186, App |
| 41 | 46.5 | 5 | 9 | US-09-871-974-2 | Sequence 2, Appli |
| 42 | 46.5 | 5 | 16 | US-10-716-293-115 | Sequence 115, App |
| 43 | 46.5 | 6 | 9 | US-09-871-974-5 | Sequence 5, Appli |
| 44 | 46.5 | 7 | 9 | US-09-845-667-2 | Sequence 2, Appli |
| 45 | 46.5 | 7 | 9 | US-09-871-974-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1
US-09-765-614B-6
; Sequence 6, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/KIaverness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-765-614B-6

Query Match 72.1%; Score 31; DB 9; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPRAAI 7
Db 2 QPRAAI 8

RESULT 2
US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:

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; APPLICANT: Nymed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
; OTHER INFORMATION: peptide
US-09-925-715-2

Query Match          72.1%; Score 31; DB 9; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
   |||||
Db 2 QPPRAAI 8

RESULT 3
US-09-999-724-58
; Sequence 58, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-58

Query Match          72.1%; Score 31; DB 10; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
   |||||
Db 2 QPPRAAI 8

RESULT 4
US-09-829-382-11
; Sequence 11, Application US/09829382
; Publication No. US20030175293A1
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
```

```
; Rosenow, Carsten I.
; Tuomanen, Elaine
; Wizenann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,382
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,065
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-829-382-11

Query Match          72.1%; Score 31; DB 10; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
   |||||
Db 2 QPPRAAI 8

RESULT 5
US-10-017-193-4
; Sequence 4, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Mai Huong
; APPLICANT: Chiu, Phillip
; TITLE OF INVENTION: Surface Coating Method and Coated Device
; FILE REFERENCE: 52200-8010
; CURRENT APPLICATION NUMBER: US/10/017,193
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attachment peptide from fibronectin
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US-10-017-193-4

Query Match 72.1%; Score 31; DB 14; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 6
US-10-722-075-6
; Sequence 6, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-10-722-075-6

Query Match 72.1%; Score 31; DB 16; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 QPPRAI 8

RESULT 7
US-09-765-614B-3
; Sequence 3, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Heparin-binding
; OTHER INFORMATION: peptide
US-09-765-614B-3

Query Match 65.1%; Score 28; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 8
US-10-722-075-3
; Sequence 3, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Heparin-binding
; OTHER INFORMATION: peptide
US-10-722-075-3

Query Match 65.1%; Score 28; DB 16; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 9
US-10-286-457-92
; Sequence 92, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-92

Query Match 58.1%; Score 25; DB 14; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRA 5
:|||||
Db 1 QPPRS 5

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RESULT 10
US-10-346-737A-6
; Sequence 6, Application US/10346737A
; Publication No. US20040142379A1
; GENERAL INFORMATION:
; APPLICANT: St. Hilaire, Phaedria
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
; FILE REFERENCE: 11225.16US01
; CURRENT APPLICATION NUMBER: US/10/346.737A
; CURRENT FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Spacer
US-10-346-737A-6

Query Match 55.8%; Score 24; DB 16; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRA 5
Db 3 RPPRA 7

RESULT 11
US-09-954-385-360
; Sequence 360, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzkv, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 360
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-360

Query Match 53.5%; Score 23; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPRA 5
Db 4 PPRA 7

RESULT 12
US-10-021-660-90
; Sequence 90, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.

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; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 019501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nuclear target motif
US-10-021-660-90

Query Match 53.5%; Score 23; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPRA 5
Db 1 PPRA 4

RESULT 13
US-09-845-667-6
; Sequence 6, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; APPLICANT: Alessi, Dario
; APPLICANT: Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:

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/ TELEPHONE: 716-393-3002
/ TELEFAX: 716-393-3001
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-845-667-6

Query Match          51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7

RESULT 14
US-09-845-667-21
; Sequence 21, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
;           Alessi, Dario
;           Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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/ SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-845-667-21

Query Match          51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7

RESULT 15
US-09-845-667-56
; Sequence 56, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
;           Alessi, Dario
;           Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-845-667-56

Query Match          51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7
/
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Wed Jul 28 09:31:26 2004

seq3.closed.rapb

Page 6

Db 2 PRAATF 7

Search completed: July 28, 2004, 08:00:13
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:52:54 ; Search time 18 Seconds
(without alignments)
22.945 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qprraay 8

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 2 | 31 | 72.1 | 8 | 1 | US-07-980-296-3 |
| 3 | 31 | 72.1 | 8 | 2 | US-08-480-333A-3 |
| 4 | 31 | 72.1 | 8 | 2 | US-08-699-965-2 |
| 5 | 31 | 72.1 | 8 | 2 | US-08-435-149-6 |
| 6 | 31 | 72.1 | 8 | 2 | US-09-025-706-10 |
| 7 | 31 | 72.1 | 8 | 3 | US-08-394-748A-13 |
| 8 | 31 | 72.1 | 8 | 3 | US-08-916-913A-3 |
| 9 | 31 | 72.1 | 8 | 3 | US-09-025-822-10 |
| 10 | 31 | 72.1 | 8 | 3 | US-08-847-065-11 |
| 11 | 31 | 72.1 | 8 | 3 | US-08-960-054A-6 |
| 12 | 31 | 72.1 | 8 | 3 | US-08-958-993A-6 |
| 13 | 31 | 72.1 | 8 | 4 | US-08-959-206A-2 |
| 14 | 31 | 72.1 | 8 | 4 | US-09-101-751A-58 |
| 15 | 31 | 72.1 | 8 | 4 | US-09-591-564-3 |
| 16 | 31 | 72.1 | 8 | 4 | US-09-925-715-2 |
| 17 | 31 | 72.1 | 8 | 5 | PCT-US93-11781-3 |
| 18 | 31 | 72.1 | 8 | 5 | PCT-US95-03478-13 |
| 19 | 28 | 65.1 | 6 | 1 | US-08-704-170-89 |
| 20 | 28 | 65.1 | 6 | 5 | PCT-US94-02631-89 |
| 21 | 28 | 65.1 | 7 | 1 | US-08-127-499A-7 |
| 22 | 28 | 65.1 | 7 | 1 | US-08-482-847-7 |
| 23 | 28 | 65.1 | 8 | 3 | US-08-960-054A-3 |
| 24 | 28 | 65.1 | 8 | 3 | US-08-958-993A-3 |
| 25 | 25 | 58.1 | 7 | 1 | US-08-127-499A-25 |
| 26 | 25 | 58.1 | 7 | 1 | US-08-482-847-25 |
| 27 | 24 | 55.8 | 7 | 1 | US-08-127-499A-3 |

28 24 55.8 7 1 US-08-482-847-3 Sequence 3, Appli
29 22 51.2 8 4 US-09-245-764-4 Sequence 4, Appli
30 21 48.8 6 1 US-08-127-499A-22 Sequence 22, Appli
31 21 48.8 6 1 US-08-482-847-22 Sequence 22, Appli
32 21 48.8 7 2 US-08-769-745-33 Sequence 33, Appli
33 21 48.8 8 2 US-08-737-085A-6 Sequence 6, Appli
34 21 48.8 8 3 US-09-246-258-6 Sequence 6, Appli
35 21 48.8 8 3 US-09-532-106-6 Sequence 6, Appli
36 21 48.8 8 4 US-09-839-666-6 Sequence 6, Appli
37 20 46.5 4 1 US-08-171-737-3 Sequence 3, Appli
38 20 46.5 4 1 US-08-202-178-9 Sequence 9, Appli
39 20 46.5 4 1 US-08-713-484-9 Sequence 9, Appli
40 20 46.5 4 2 US-08-955-263-9 Sequence 9, Appli
41 20 46.5 4 2 US-08-232-539D-46 Sequence 46, Appli
42 20 46.5 4 3 US-08-466-151-59 Sequence 59, Appli
43 20 46.5 4 4 US-08-466-163B-59 Sequence 59, Appli
44 20 46.5 4 4 US-09-802-096-59 Sequence 59, Appli
45 20 46.5 5 1 US-08-171-737-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "FNS (1892-1899)

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OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-291-349A-5
Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

RESULT 2
US-07-990-296-3
; Sequence 3, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; TITLE OF INVENTION: with Fibronectin Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 kD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronectin
; LOCATION: Represents isolated fibronectin
; LOCATION: residues 1892-1899 from all plasma isoforms
; LOCATION: of fibronectin
US-07-990-296-3
Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-480-133A-3
; Sequence 3, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey B.
; TITLE OF INVENTION: Method for Treating Inflammatory
; TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-133A-3
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-699-965-2
; Sequence 2, Application US/08699965
; Patent No. 5853744
; GENERAL INFORMATION:
; APPLICANT: MOORADIAN, DANIEL L.
; APPLICANT: FIELDS, GREGG B.
; TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE
; TITLE OF INVENTION: TO INCLUDE A BIOMOLECULE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```



```

; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NO. 5853/44th Fourth Street, Suite 203
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,965
; FILING DATE: 20-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00300101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-699-965-2

```

```

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 QPPRAAI 7
Db 2 QPPRAAI 8

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```

RESULT 5
US-08-435-149-6
; Sequence 6, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABEL A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAP PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585

```

```

; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-435-149-6
; Query Match 72.1%; Score 31; DB 2; Length 8;
; Best Local Similarity 85.7%; Pred. No. 3e+05;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; Qy 1 QPPRAAI 7
; Db 2 QPPRAAI 8

```

```

RESULT 6
US-09-025-706-10
; Sequence 10, Application US/09025706
; Patent No. 5958874
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Greiling, Doris
; APPLICANT: Gallit, James
; TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
; TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-025-706-10

```

```

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 QPPRAAI 7
Db 2 QPPRAAI 8

```

```

RESULT 7

```

US-08-394-748A-13
; Sequence 13, Application US/08394748A
; Patent No. 6013628
; GENERAL INFORMATION:
; APPLICANT: Skubitz, Amy P.N.
; APPLICANT: Furght Leo T.
; APPLICANT: Balles, Mark
; APPLICANT: Gregerson, Dale S.
; APPLICANT: Agarwal, Anita
; APPLICANT: Wright, Martha M.
; APPLICANT: Murali, Shobana
; TITLE OF INVENTION: Method for Treating Conditions of the Eye
; TITLE OF INVENTION: Using Polypeptides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6013628west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,748A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/203,458
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600.307US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; STRAIN: FN-C/H-V
US-08-394-748A-13

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 8
US-08-916-913A-3
; Sequence 3, Application US/08916913A
; Patent No. 6121027
; GENERAL INFORMATION:
; APPLICANT: Clapper, David L.
; APPLICANT: Swanson, Melvin J.
; APPLICANT: Hu, Sheau-Ping
; APPLICANT: Amos, Richard A.
; APPLICANT: Everson, Terrence P.
; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOIETIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fredrikson & Byron, P.A.
; STREET: 900 Second Avenue South
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-3397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows-97
; SOFTWARE: ASCII files
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,913A
; FILING DATE: 15 August 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-913A-3

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 9
US-09-025-622-10
; Sequence 10, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Greiling, Doris
; TITLE OF INVENTION: FIBROECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramer, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-10

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRAI 8

RESULT 10
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizenmann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-847-065-11

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRAI 8

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DB 2 QPPRAI 8

RESULT 11
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-960-054A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRAI 8

RESULT 12
US-08-958-993A-6
; Sequence 6, Application US/08958993A
; Patent No. 6264917
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/993
; CURRENT APPLICATION NUMBER: US/08/958,993A
; CURRENT FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-958-993A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRAI 8

RESULT 13
US-08-959-206A-2
; Sequence 2, Application US/08959206A
; Patent No. 6331289
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS

```

;; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
;; TITLE OF INVENTION: agents
;; FILE REFERENCE: REF/Klaveness/206
;; CURRENT APPLICATION NUMBER: US/08/959,206A
;; CURRENT FILING DATE: 1997-10-24
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
;; OTHER INFORMATION: peptide

US-08-959-206A-2

Query Match 72.1%; Score 31; DB 4; Length 8;

Best Local Similarity 85.7%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

Db 2 QPPRAI 8

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Swanson, Melvin J.
Hu, Sheau-Ping
Amos, Richard A.
Everson, Terrence P.
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY
ACTIVE MOIETIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fredrikson & Byron, P.A.

STREET: 900 Second Avenue South

CITY: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55402-3397

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows-97

SOFTWARE: ASCII files

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/591,564

FILING DATE: 09-Jun-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/916,913

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Philip M.

REGISTRATION NUMBER: 31,162

REFERENCE/DOCKET NUMBER: 9896.116.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 347-7088

TELEFAX: (612) 347-7077

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acid residues

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-591-564-3

Query Match 72.1%; Score 31; DB 4; Length 8;

Best Local Similarity 85.7%; Pred. No. 3e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

Db 2 QPPRAI 8

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Search completed: July 28, 2004, 07:55:51

Job time: 18 secs

Query Match 72.1%; Score 31; DB 4; Length 8;

Best Local Similarity 85.7%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

Db 2 QPPRAI 8

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RESULT 15

US-09-591-564-3

; Sequence 3, Application US/09591564

; Patent No. 6514734

; GENERAL INFORMATION:

; APPLICANT: Clapper, David L.